

Abstract

A sample of normal tissue specimens obtained from a subset of a population of subjects with shared characteristics is profiled in order to generate a plurality of structural indices that correspond to statistically significant representations of characteristics of tissue associated with the population. The structural indices include cell density, matrix density, blood vessel density and layer thickness. Alternatively, the sample of normal tissue specimens obtained from the subset of the population of subjects with shared characteristics can also be profiled in order to generate a plurality of cell function and/or mechanical indices that correspond to statistically significant representations of characteristics of tissue associated with the population. Structural, mechanical and/or cell function indices for a plurality of tissue populations are determined, and then stored in a database. The database information is then used to classify tissue specimens (e.g., human tissue specimens, animal tissue specimens, plant tissue specimens, food tissue specimens, or manufactured tissue specimens) provided by a user. In particular, a user measures parameters (e.g., structural, mechanical and/or cell function indices) associated with the user's tissue specimens and then compares this information to corresponding parameters for normal tissue in the database in order to classify the user's tissue specimens as either normal or abnormal.